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catgatcatg	gggctgcagg	aattcgatgg	tcgaatttgc	tttcgaattt	ctgccattca	5160
tccgcttatt	atcacttatt	caggcgtagc	accaggcggt	taagggcacc	aataactgcc	5220
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tctgccgaca	tggaagccat	cacagacggc	atgatgaacc	tgaatcgcca	gcggcatcag	5340
caccttgctg	ccttgcgat	aatatttgcc	catggtgaaa	acgggggcga	agaagttgtc	5400
catattggcc	acgttttaaat	caaaaactggt	gaaactcacc	cagggattgg	ctgagacgaa	5460
aaacatatct	tcaataaacc	ctttagggaa	ataggccagg	ttttaccctg	aacacgccac	5520
atcttgcgaa	tatatgtgta	gaaactgccg	gaaatcgctg	tggtattcac	tccagagcga	5580
tgaaaacggt	tcagtttgct	catggaaaac	ggtgtaacaa	gggtgaacac	tatcccatat	5640
caccagctca	ccgtctttca	ttgccatacg				5670

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 <223> LacZ(/chitobiase Fusion

<220>
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 <222> (44)...(50)
 <223> Lac promoter

<221> -10_signal
 <222> (69)...(74)
 <223> Lac promoter
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 <222> (81)...(107)
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<221> protein_bind
 <222> (7)...(34)
 <223> CAP-cAMP binding site

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 ccggtcgta tgttgtgtgg aattgtgagc ggataacaat ttcacacagg aaacagct 118
 atg acc atg att acg cca agc ttg cat gcc tgc agg tcg act cta gag 166
 Met Thr Met Ile Thr Pro Ser Leu His Ala Cys Arg Ser Thr Leu Glu
 1 5 10 15

gat ccc cgg gta ccg agc tct gag caa caa gtt gta aac tca ctg gct 214
 Asp Pro Arg Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala
 20 25 30

gat aac ctt gat atc caa tat gaa 238
 Asp Asn Leu Asp Ile Gln Tyr Glu
 35 40

<210> 16
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 <212> PRT
 <213> Artificial Sequence
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 <223> LacZ(/chitobiase Fusion

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 1 5 10 15
 Asp Pro Arg Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala
 20 25 30
 Asp Asn Leu Asp Ile Gln Tyr Glu
 35 40

<210> 17
 <211> 22
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> dnaA/chitobiase Fusion

<400> 17
 Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
 1 5 10 15
 Leu Val Pro Ser Ser Glu
 20

<210> 18
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09630931-030200

<212> DNA
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<220>
<221> CDS
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<223> dnaA/Chitobiase Fusion

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1 5 10 15

ttg gta ccg agc tct gag caa caa gtt gta aac tca ctg gct gat aac 96
Leu Val Pro Ser Ser Glu Gln Gln Val Val Asn Ser Leu Ala Asp Asn
20 25 30

ctt gat atc caa tat gaa gtg tta act aac cat ggt gct aac gaa ggt 144
Leu Asp Ile Gln Tyr Glu Val Leu Thr Asn His Gly Ala Asn Glu Gly
35 40 45

ctt gcg tgc caa gat atg ggc gca gaa tgg gct tct tgt aac aaa gta 192
Leu Ala Cys Gln Asp Met Gly Ala Glu Trp Ala Ser Cys Asn Lys Val
50 55 60

aac atg acg ctt gtt aac caa ggt gaa gct gtt gac tca aaa gat tgg 240
Asn Met Thr Leu Val Asn Gln Gly Glu Ala Val Asp Ser Lys Asp Trp
65 70 75 80

gct att tac ttc cac agc att cgt ctg att ctg gat gtt gac aac gag 288
Ala Ile Tyr Phe His Ser Ile Arg Leu Ile Leu Asp Val Asp Asn Glu
85 90 95

cag ttc aaa atc tct cgt gta acg ggt gac cta cat aag cta gaa cca 336
Gln Phe Lys Ile Ser Arg Val Thr Gly Asp Leu His Lys Leu Glu Pro
100 105 110

aca gat aag ttt gac ggc ttc gct gcc ggt gaa gag gtt gtt ctt cca 384
Thr Asp Lys Phe Asp Gly Phe Ala Ala Gly Glu Glu Val Val Leu Pro
115 120 125

ttg gtt ggt gaa tac tgg caa cta ttt gaa act gac ttc atg ccg ggt 432
Leu Val Gly Glu Tyr Trp Gln Leu Phe Glu Thr Asp Phe Met Pro Gly
130 135 140

gca ttc gtt tct gct cca aac gca gaa cct aag atg att gct tct cta 480
Ala Phe Val Ser Ala Pro Asn Ala Glu Pro Lys Met Ile Ala Ser Leu
145 150 155 160

aat act gaa gat gtt gcg tct ttt gtg acg ggt ctt gaa ggt aac aac 528
Asn Thr Glu Asp Val Ala Ser Phe Val Thr Gly Leu Glu Gly Asn Asn
165 170 175

cta aaa cgt aca cca gat gac aac aat gta ttt gca aac gct gtg tct 576
Leu Lys Arg Thr Pro Asp Asp Asn Asn Val Phe Ala Asn Ala Val Ser
180 185 190

0022080" TEE60E950

00630931-080200

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tta cta cca aca cca atg cac gtt gaa gcg ggt aaa ggc aaa gta gat Leu Leu Pro Thr Pro Met His Val Glu Ala Gly Lys Gly Lys Val Asp 210 215 220	672
atc gcg gat ggt att gcg ctg cct aaa gac gca ttc gat gcg act cag Ile Ala Asp Gly Ile Ala Leu Pro Lys Asp Ala Phe Asp Ala Thr Gln 225 230 235 240	720
ttc gca gcg att caa gat cgt gca gaa gtg gta ggt gtg gac gtt cgt Phe Ala Ala Ile Gln Asp Arg Ala Glu Val Val Gly Val Asp Val Arg 245 250 255	768
ggt gat ctt cct gta agc atc act gtt gtt cct gca gac ttc acc ggt Gly Asp Leu Pro Val Ser Ile Thr Val Val Pro Ala Asp Phe Thr Gly 260 265 270	816
gaa tta gca aaa tct ggt gct tac gaa atg agc atc aaa ggc gac ggt Glu Leu Ala Lys Ser Gly Ala Tyr Glu Met Ser Ile Lys Gly Asp Gly 275 280 285	864
att gtg att aaa gcg ttc gac caa gca ggc gct ttc tac gca gta caa Ile Val Ile Lys Ala Phe Asp Gln Ala Gly Ala Phe Tyr Ala Val Gln 290 295 300	912
tct atc ttt ggc ctg gta gat agc caa aat gct gat tct cta cca caa Ser Ile Phe Gly Leu Val Asp Ser Gln Asn Ala Asp Ser Leu Pro Gln 305 310 315 320	960
ctg tct att aaa gat gcg cct cgt ttt gat tac cgt ggt gtg atg gtg Leu Ser Ile Lys Asp Ala Pro Arg Phe Asp Tyr Arg Gly Val Met Val 325 330 335	1008
gat gtg gct cgt aac ttc cac tct aag gac gca atc ctt gca acg cta Asp Val Ala Arg Asn Phe His Ser Lys Asp Ala Ile Leu Ala Thr Leu 340 345 350	1056
gac caa atg gca gcg tac aag atg aac aaa ctt cac ctt cac cta acc Asp Gln Met Ala Ala Tyr Lys Met Asn Lys Leu His Leu His Leu Thr 355 360 365	1104
gat gat gaa ggc tgg cgt tta gaa atc ccg ggt ctg cct gag ctg aca Asp Asp Glu Gly Trp Arg Leu Glu Ile Pro Gly Leu Pro Glu Leu Thr 370 375 380	1152
gaa gtg ggt gct aac cgt tgt ttc gat aca caa gag aaa agc tgt tta Glu Val Gly Ala Asn Arg Cys Phe Asp Thr Gln Glu Lys Ser Cys Leu 385 390 395 400	1200
ctg cct cag ctt ggc tct ggt cca acg aca gac aac ttt ggc tct ggc Leu Pro Gln Leu Gly Ser Gly Pro Thr Thr Asp Asn Phe Gly Ser Gly 405 410 415	1248

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cgt aac att gaa gtg att cca gaa atc gat atg cca gct cac gct cgt Arg Asn Ile Glu Val Ile Pro Glu Ile Asp Met Pro Ala His Ala Arg 435 440 445	1344
gca gca gta gta tca atg gaa gct cgt tac gac cgc cta atg gaa gaa Ala Ala Val Val Ser Met Glu Ala Arg Tyr Asp Arg Leu Met Glu Glu 450 455 460	1392
ggc aaa gaa gct gaa gcg aac gaa tac cgt ctg atg gat cct caa gat Gly Lys Glu Ala Glu Ala Asn Glu Tyr Arg Leu Met Asp Pro Gln Asp 465 470 475 480	1440
aca tca aac gta acg acg gtt cag ttc tac aat aag caa agc ttc atc Thr Ser Asn Val Thr Thr Val Gln Phe Tyr Asn Lys Gln Ser Phe Ile 485 490 495	1488
aac cca tgt atg gaa tct tca act cgc ttt gtt gat aag gtg att tca Asn Pro Cys Met Glu Ser Ser Thr Arg Phe Val Asp Lys Val Ile Ser 500 505 510	1536
gaa gtg gca gca atg cac caa gaa gct ggc gct cca cta aca act tgg Glu Val Ala Ala Met His Gln Glu Ala Gly Ala Pro Leu Thr Thr Trp 515 520 525	1584
cac ttc ggt ggt gac gaa gcg aag aac atc aag cta ggt gct ggt ttc His Phe Gly Gly Asp Glu Ala Lys Asn Ile Lys Leu Gly Ala Gly Phe 530 535 540	1632
caa gac gtt aac gca gaa gat aaa gta agc tgg aaa ggc acg att gac Gln Asp Val Asn Ala Glu Asp Lys Val Ser Trp Lys Gly Thr Ile Asp 545 550 555 560	1680
ctg tct aaa caa gac aag ccg ttt gca cag tct cca caa tgt cag acg Leu Ser Lys Gln Asp Lys Pro Phe Ala Gln Ser Pro Gln Cys Gln Thr 565 570 575	1728
cta atc aca gat ggc aca gtc agt gac ttt gct cac cta cca agc cac Leu Ile Thr Asp Gly Thr Val Ser Asp Phe Ala His Leu Pro Ser His 580 585 590	1776
ttc gcg gaa gaa gtg tcg aag att gtt gct gag aaa ggc att cca aac Phe Ala Glu Glu Val Ser Lys Ile Val Ala Glu Lys Gly Ile Pro Asn 595 600 605	1824
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ttc gct aca gaa aat act cgc gta aac ttc tgg gac gtt ctg tac tgg Phe Ala Thr Glu Asn Thr Arg Val Asn Phe Trp Asp Val Leu Tyr Trp 625 630 635 640	1920
ggc ggt act tcc tca gtg tac gag tgg tct aag aaa ggt tac gac gtg	1968

002030" T E 6 0 E 9 6 0

Gly Gly Thr Ser Ser Val Tyr Glu Trp Ser Lys Lys Gly Tyr Asp Val	
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att gtt tct aac cca gat tac gtg tac atg gat atg cca tac gaa gtt	2016
Ile Val Ser Asn Pro Asp Tyr Val Tyr Met Asp Met Pro Tyr Glu Val	
660 665 670	
gac ccg aaa gag cgt ggt tac tac tgg gca aca cgt gca acg gat act	2064
Asp Pro Lys Glu Arg Gly Tyr Tyr Trp Ala Thr Arg Ala Thr Asp Thr	
675 680 685	
cgt aag atg ttt ggc ttt gca cca gag aac atg cct caa aac gca gaa	2112
Arg Lys Met Phe Gly Phe Ala Pro Glu Asn Met Pro Gln Asn Ala Glu	
690 695 700	
act tct gta gat cgc gat ggc aat ggc ttt act ggt aaa ggt gaa atc	2160
Thr Ser Val Asp Arg Asp Gly Asn Gly Phe Thr Gly Lys Gly Glu Ile	
705 710 715 720	
gaa gcg aaa cct ttc tac ggt cta tct gca caa ctt tgg tct gag aca	2208
Glu Ala Lys Pro Phe Tyr Gly Leu Ser Ala Gln Leu Trp Ser Glu Thr	
725 730 735	
gta cgt aac gac gag caa tac gag tac atg gta ttc cct cgc gtc ctc	2256
Val Arg Asn Asp Glu Gln Tyr Glu Tyr Met Val Phe Pro Arg Val Leu	
740 745 750	
gct gct gct cag cgt gca tgg cac cgt gct gac tgg gaa aac gac tac	2304
Ala Ala Ala Gln Arg Ala Trp His Arg Ala Asp Trp Glu Asn Asp Tyr	
755 760 765	
aaa gtt ggt gtt gag tac tcg caa aac tct aat cta gtt gat aaa gca	2352
Lys Val Gly Val Glu Tyr Ser Gln Asn Ser Asn Leu Val Asp Lys Ala	
770 775 780	
tcg cta aac caa gac tac aac cgc ttt gcg aac gta ctt ggt caa cgt	2400
Ser Leu Asn Gln Asp Tyr Asn Arg Phe Ala Asn Val Leu Gly Gln Arg	
785 790 795 800	
gaa ctg gct aag cta gaa aaa tca ggt att gac tac cgc cta cca gta	2448
Glu Leu Ala Lys Leu Glu Lys Ser Gly Ile Asp Tyr Arg Leu Pro Val	
805 810 815	
cca ggt gca aaa gta gaa gat ggt aag cta gca atg aac gtt cag ttc	2496
Pro Gly Ala Lys Val Glu Asp Gly Lys Leu Ala Met Asn Val Gln Phe	
820 825 830	
cct ggc gta acg ctt caa tac tct ctg gat ggt gag aac tgg ttg act	2544
Pro Gly Val Thr Leu Gln Tyr Ser Leu Asp Gly Glu Asn Trp Leu Thr	
835 840 845	
tat gca gac aac gct cgt cca aat gta act ggt gaa gtc ttc atc cgc	2592
Tyr Ala Asp Asn Ala Arg Pro Asn Val Thr Gly Glu Val Phe Ile Arg	
850 855 860	
tcg gta tct gcg aca ggt gag aag gta agc cgt atc act agc gtg aaa	2640
Ser Val Ser Ala Thr Gly Glu Lys Val Ser Arg Ile Thr Ser Val Lys	

865

870

875

880

2643

taa

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<210> 19

<211> 880

<212> PRT

<213> Artificial Sequence

<220>

<223> dnaA/Chitobiase Fusion

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 Leu Asp Ile Gln Tyr Glu Val Leu Thr Asn His Gly Ala Asn Glu Gly
 35 40 45
 Leu Ala Cys Gln Asp Met Gly Ala Glu Trp Ala Ser Cys Asn Lys Val
 50 55 60
 Asn Met Thr Leu Val Asn Gln Gly Glu Ala Val Asp Ser Lys Asp Trp
 65 70 75 80
 Ala Ile Tyr Phe His Ser Ile Arg Leu Ile Leu Asp Val Asp Asn Glu
 85 90 95
 Gln Phe Lys Ile Ser Arg Val Thr Gly Asp Leu His Lys Leu Glu Pro
 100 105 110
 Thr Asp Lys Phe Asp Gly Phe Ala Ala Gly Glu Glu Val Val Leu Pro
 115 120 125
 Leu Val Gly Glu Tyr Trp Gln Leu Phe Glu Thr Asp Phe Met Pro Gly
 130 135 140
 Ala Phe Val Ser Ala Pro Asn Ala Glu Pro Lys Met Ile Ala Ser Leu
 145 150 155 160
 Asn Thr Glu Asp Val Ala Ser Phe Val Thr Gly Leu Glu Gly Asn Asn
 165 170 175
 Leu Lys Arg Thr Pro Asp Asp Asn Asn Val Phe Ala Asn Ala Val Ser
 180 185 190
 Arg Phe Glu Lys Asn Glu Asp Leu Ala Thr Gln Asp Val Ser Thr Thr
 195 200 205
 Leu Leu Pro Thr Pro Met His Val Glu Ala Gly Lys Gly Lys Val Asp
 210 215 220
 Ile Ala Asp Gly Ile Ala Leu Pro Lys Asp Ala Phe Asp Ala Thr Gln
 225 230 235 240
 Phe Ala Ala Ile Gln Asp Arg Ala Glu Val Val Gly Val Asp Val Arg
 245 250 255
 Gly Asp Leu Pro Val Ser Ile Thr Val Val Pro Ala Asp Phe Thr Gly
 260 265 270
 Glu Leu Ala Lys Ser Gly Ala Tyr Glu Met Ser Ile Lys Gly Asp Gly
 275 280 285
 Ile Val Ile Lys Ala Phe Asp Gln Ala Gly Ala Phe Tyr Ala Val Gln
 290 295 300
 Ser Ile Phe Gly Leu Val Asp Ser Gln Asn Ala Asp Ser Leu Pro Gln
 305 310 315 320
 Leu Ser Ile Lys Asp Ala Pro Arg Phe Asp Tyr Arg Gly Val Met Val
 325 330 335
 Asp Val Ala Arg Asn Phe His Ser Lys Asp Ala Ile Leu Ala Thr Leu

002030"TE50E960

002080-TE60E950

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355										360					365						
Asp	Asp	Glu	Gly	Trp	Arg	Leu	Glu	Ile	Pro	Gly	Leu	Pro	Glu	Leu	Thr						
370										375					380						
Glu	Val	Gly	Ala	Asn	Arg	Cys	Phe	Asp	Thr	Gln	Glu	Lys	Ser	Cys	Leu						
385										390					395						
Leu	Pro	Gln	Leu	Gly	Ser	Gly	Pro	Thr	Thr	Asp	Asn	Phe	Gly	Ser	Gly						
405										410					415						
Tyr	Phe	Ser	Lys	Ala	Asp	Tyr	Val	Glu	Ile	Leu	Lys	Tyr	Ala	Lys	Ala						
420										425					430						
Arg	Asn	Ile	Glu	Val	Ile	Pro	Glu	Ile	Asp	Met	Pro	Ala	His	Ala	Arg						
435										440					445						
Ala	Ala	Val	Val	Ser	Met	Glu	Ala	Arg	Tyr	Asp	Arg	Leu	Met	Glu	Glu						
450										455					460						
Gly	Lys	Glu	Ala	Glu	Ala	Asn	Glu	Tyr	Arg	Leu	Met	Asp	Pro	Gln	Asp						
465										470					475						
Thr	Ser	Asn	Val	Thr	Thr	Val	Gln	Phe	Tyr	Asn	Lys	Gln	Ser	Phe	Ile						
485										490					495						
Asn	Pro	Cys	Met	Glu	Ser	Ser	Thr	Arg	Phe	Val	Asp	Lys	Val	Ile	Ser						
500										505					510						
Glu	Val	Ala	Ala	Met	His	Gln	Glu	Ala	Gly	Ala	Pro	Leu	Thr	Thr	Trp						
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His	Phe	Gly	Gly	Asp	Glu	Ala	Lys	Asn	Ile	Lys	Leu	Gly	Ala	Gly	Phe						
530										535					540						
Gln	Asp	Val	Asn	Ala	Glu	Asp	Lys	Val	Ser	Trp	Lys	Gly	Thr	Ile	Asp						
545										550					555						
Leu	Ser	Lys	Gln	Asp	Lys	Pro	Phe	Ala	Gln	Ser	Pro	Gln	Cys	Gln	Thr						
565										570					575						
Leu	Ile	Thr	Asp	Gly	Thr	Val	Ser	Asp	Phe	Ala	His	Leu	Pro	Ser	His						
580										585					590						
Phe	Ala	Glu	Glu	Val	Ser	Lys	Ile	Val	Ala	Glu	Lys	Gly	Ile	Pro	Asn						
595										600					605						
Phe	Gln	Ala	Trp	Gln	Asp	Gly	Leu	Lys	Tyr	Ser	Asp	Gly	Glu	Lys	Ala						
610										615					620						
Phe	Ala	Thr	Glu	Asn	Thr	Arg	Val	Asn	Phe	Trp	Asp	Val	Leu	Tyr	Trp						
625										630					635						
Gly	Gly	Thr	Ser	Ser	Val	Tyr	Glu	Trp	Ser	Lys	Lys	Gly	Tyr	Asp	Val						
645										650					655						
Ile	Val	Ser	Asn	Pro	Asp	Tyr	Val	Tyr	Met	Asp	Met	Pro	Tyr	Glu	Val						
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675										680					685						
Arg	Lys	Met	Phe	Gly	Phe	Ala	Pro	Glu	Asn	Met	Pro	Gln	Asn	Ala	Glu						
690										695					700						
Thr	Ser	Val	Asp	Arg	Asp	Gly	Asn	Gly	Phe	Thr	Gly	Lys	Gly	Glu	Ile						
705										710					715						
Glu	Ala	Lys	Pro	Phe	Tyr	Gly	Leu	Ser	Ala	Gln	Leu	Trp	Ser	Glu	Thr						
725										730					735						
Val	Arg	Asn	Asp	Glu	Gln	Tyr	Glu	Tyr	Met	Val	Phe	Pro	Arg	Val	Leu						
740										745					750						
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755										760					765						
Lys	Val	Gly	Val	Glu	Tyr	Ser	Gln	Asn	Ser	Asn	Leu	Val	Asp	Lys	Ala						
770										775					780						
Ser	Leu	Asn	Gln	Asp	Tyr	Asn	Arg	Phe	Ala	Asn	Val	Leu	Gly	Gln	Arg						
785										790					795						

Glu Leu Ala Lys Leu Glu Lys Ser Gly Ile Asp Tyr Arg Leu Pro Val
 805 810 815
 Pro Gly Ala Lys Val Glu Asp Gly Lys Leu Ala Met Asn Val Gln Phe
 820 825 830
 Pro Gly Val Thr Leu Gln Tyr Ser Leu Asp Gly Glu Asn Trp Leu Thr
 835 840 845
 Tyr Ala Asp Asn Ala Arg Pro Asn Val Thr Gly Glu Val Phe Ile Arg
 850 855 860
 Ser Val Ser Ala Thr Gly Glu Lys Val Ser Arg Ile Thr Ser Val Lys
 865 870 875 880

18

1

002030-TE60E960